My Pipeline

Overview

```
$ perl rna_seq_pipeline.pl -help

USAGE:
        perl rna_seq_pipeline.pl -i <INPUT> -o <OUTPUT> -g <GENOME> -r <RUNID> <OPTIONS>

EXAMPLE RUN:
        perl rna_seq_pipeline.pl -i /home/kanagarajm/samples_fq/ -o /mnt/state_lab/share/Manoj/rna_seq_out/ -g u -r 81214 --pairedEnd

REQUIRED ARGUMENTS:
        -i (input)                              Path to directory containing all fastq files to be run through pipeline
                                                Input fastq files within directory should be gzipped and have tags to s
```